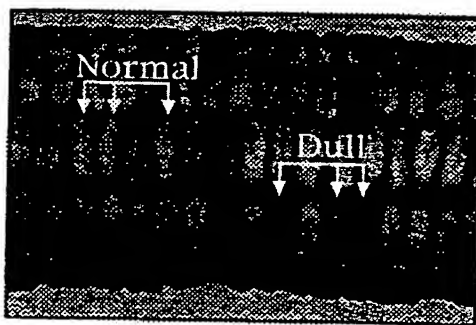


**FIGURE 1A**



**FIGURE 1B**

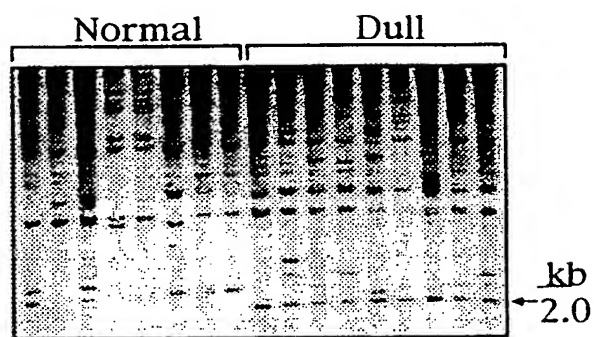


FIGURE 2A



FIGURE 2B

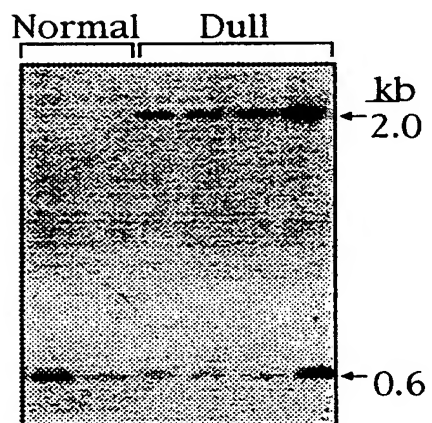


FIGURE 2C

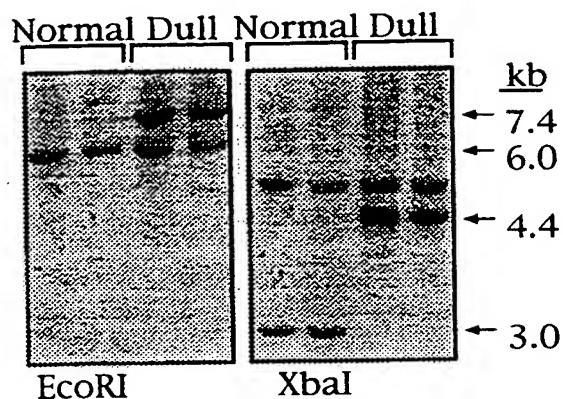
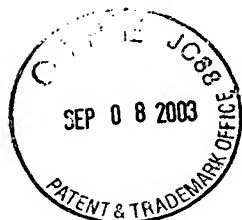


FIGURE 3A

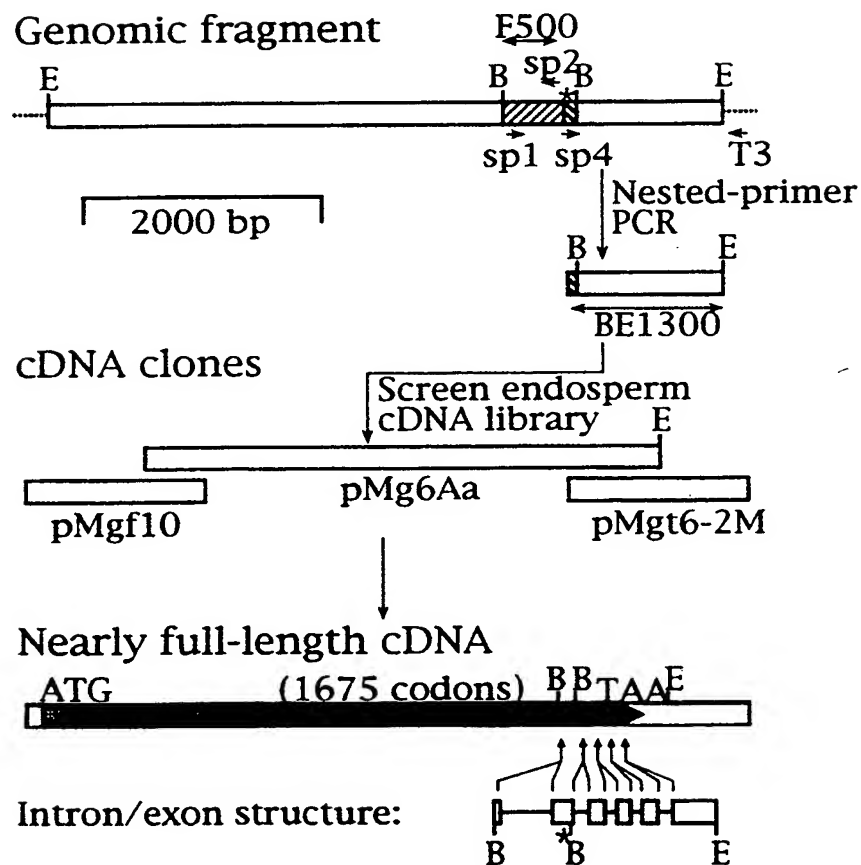


FIGURE 3B

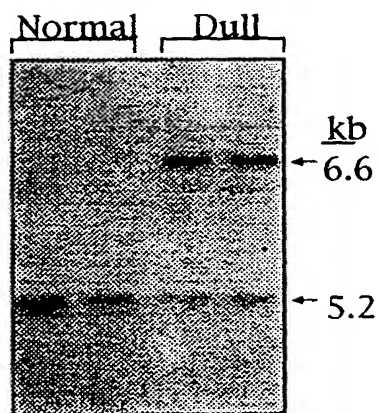


FIGURE 4

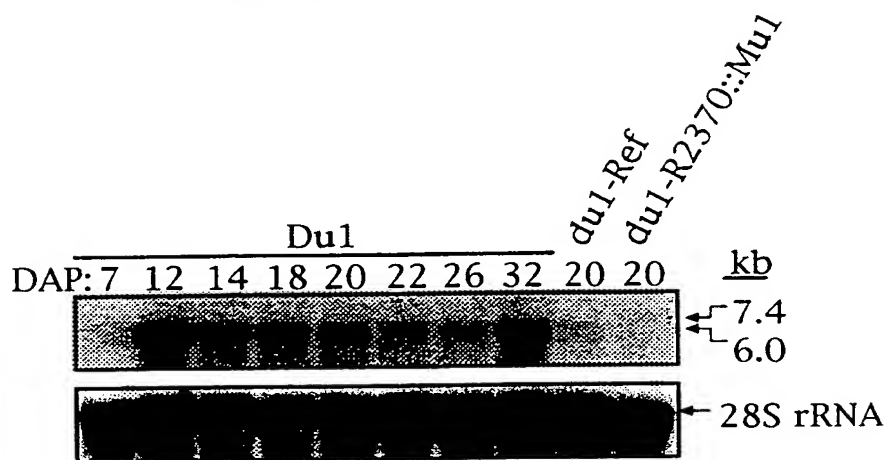


FIGURE 5A

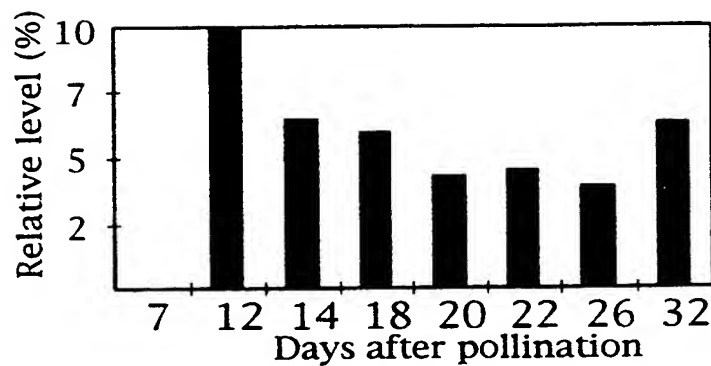


FIGURE 5B

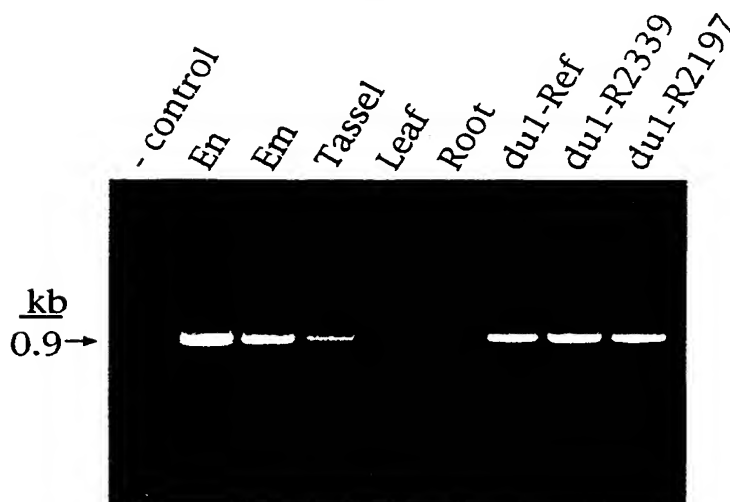


FIGURE 5C

	MEMVLRSQSPCLCLRSQPLIFRPTVAGGG	30
DU1	GTQSLRLTRFARRRVIRCVVSPGCPNRKSRRTASPNVKVAAYSNYAPRLLVSSSKKS	89
DU1	EHHSSRHREETIDTYNGLSGSDAAELTSNRDVEIEVDLQHISEEELPGKVSINASLGE	148
DU1	METVDEAEVEEDKFEVDTSGIVLRNVAVREVPKDEHNAKDVFFVVDSSGTAPDNAVEE	207
DU1	VVDEAEVEEDMVDVDILGLDLNNATIEEIDLMEEALENFVDVDSFGNASSGRTYGGVDE	266
DU1	LGELPSTSVDCIAINGKRRSLKPKPLPIVRFQEQEQIVLSIVDEEGLIASSCEEQPVV	325
DU1	DYDKQEEENSTAFDEQKQLTDDFEEGIVHFPENNDIVGSSKFLQKQELDGSYKQD	384
DU1	RSTTGLHEQDQSVVSSHGQDKSIVGVFPQIQYNDQSIAGSHRQDQSIAGAPEQIQSVAG	443
DU1	YIKPNQSIQVSCQKQHELIIPPEKKIESIISYNEIDQSIQVSHKQDKSVVSVPEQIQSIV	502
SS3	MDVFPPLHRSLSCTSVSNAITHLKPKPILGFVSHGTTLSVQSSSWRKDGMVTGVS	56
DU1	SHSKHNSITVDSYRQAESIIIGVPEKVQSITSYDKLDQSIQVSLQDEPIISVPEKIQSI	561
SS3	FSICANFSGRRRRKVVSTPRSQSSPKGFVPRKPSGMSTQKVKQSNQSGDKESKSTSTKE	115
DU1	VHYTKPNQSIQVGLPKQQQSIVHMEPKQSIDGFPKQDLSIVGTSNEFQTKQLATVGTHTD	620
SS3	SEISNQKTVEARVETSDDDTKGVMRDHFLEDEDEINGSTKSLMSPPVRVSSQFVESEE	174
DU1	GLLMKGVEAKETSQKTEGDTLQATFNVNLSQKQKQKKEADEITIEKINDEDLVMIE	679
SS3	TGGDDKDAKLNKSKRSEESGFIIDSVIREQSGSQGFIENASSKGSNAVGTCLKLYEILQVD	233

FIGURE 6A-1



DU1	EQKSIAMNEEQTI	VEIGIDKAKFL	HLISEESSW	DENEVGII	EAD	EQYE	738
SS3	VEPQQLKENNAGN	VEYKGPVASK	LEITKASDVETES	NEIDDL	DTNSFFK	SDLEDE	292
DU1	VDETSMTSEC	IQESPNDLDPQALWSMLQELAEKNYS	CKLFTY	PDVLK	ADSTIDLY		797
SS3	PLAAGTVETC	SSNLRLRLEMEANLRRQAIERLAENL	LOQIRLECFE	ENAVK	DEDEVEIF		351
DU1	FNRDL	SAVANE	PDVLTKGAFN	CKMRF	TEK	LHKSELAGDWM	856
SS3	LNRL	SLTKNESDVL	JMGAENEMRYRSET	TRLTETH	NGDWM	CKIHVPKEAYRA	410
DU1	FNGHTVY	ENNNND	VIQIESTMDEN	IFEDFLAE	EKKORE	LENLANE	915
SS3	FNGQD	VYDNN	DCNDESI	TVKGM	QIIDE	ENEL	469
DU1	MEER	ADKADR	VOAKVE	VEIKK	NKLCNV	LGLARAPV	974
SS3	IEAK	IEI	FADRAOAK	EEAAKK	KVLR	ELMVKEATKTR	528
DU1	INSR	PLVH	STEIM	HGGYNN	WIDGLS	FAERLVHHDK	1033
SS3	KSSG	PLSHAK	DLIM	HGGYNN	WKDGLS	IVKKLVKSER	587
DU1	ADGPP	GSARNY	DNN	GGHDF	HATLP	NNMT	1092
SS3	ADGPE	KHAI	AYDNN	HRQ	DFHAI	VPNHIP	646
DU1	ERN	AKMA	EMKE	KTMR	FLMSQ	HI	1151
SS3	EKT	ALL	KTE	KERT	TKSE	LLSOKH	705
DU1	CSFN	RW	MY	PG	VL	PPQKM	1210
SS3	CSFN	RW	TH	RL	CPL	PPQKM	764
DU1	DYHI	PVFG	SI	AK	EP	PMH	1269
SS3	DYHI	PVFG	V	AK	EP	PMH	823
DU1	GC	IN	LS	NV	KN	LQ	1328
SS3	DC	IK	MN	NV	KD	FR	882

FIGURE 6A-2





1387  
941  
1446  
1000  
1505  
1059  
1564  
1118  
1623  
1177  
1674  
1230

DU1	RFGFFCRSALEFLLOSGSSFNIIHCHDWSSAPVAVLHKENYAKSSLANARVFTIHNL
SS3	RFGFFCHALEFLLOSGFSDLIHCHDWSSAPVAVLHKEQYTHYCLSKSRIVFTIHNL
DU1	FGAHHITGKAMRYCDKATTVSNNTYSKEVSGHGAIMPHLGKFYGIILNGIDDPDIWDHYNDNF
SS3	FGADLIIGRAMTNADKATTVSPETYSQEVSGNPVIAAPHIHKFHGIIVNGIDDPDIWDHLDNKE
DU1	IPVHYTCENVVEGKRAAKRALQKFGIQQIDMPVVGIVTRLTAQKGIHLIKHAIHRTLE
SS3	IPVHYTCENVVEGKRAAKRALQKFGIQQIDMPVVGIVTRLTAQKGIHLIKHAIHRTLE
DU1	RNGQVLLGSAPDRIOADFVNLANIHLGVNHGQVRISLTYDEPLSHLIYAGSDFILVF
SS3	RNGQVLLGSAPDRVQNNFVNLANQLHISKYNDRARICLTDEPLSHLIYAGSDFILVF
DU1	SIFEPCGLTQLVAMRYGHIPIVRKTGGLFDTVFVDNDKERARDRGLPENGFSFDGADS
SS3	SIFEPCGLTQLVAMRYGHIPIVRKTGGLFDTVFVDNDKERARDRGLPENGFSFDGADS
DU1	NGVDYALNRATISAMWIDGRWENSLCKQVMEQDWSNRPALDYIELYRSASKL
SS3	GGVDYALNRATISAMWIDGRWENSLCKQVMEQDWSNRPALDYIELYHARKLE

DU1 (SEQ ID NO: 12)

SS3 (SEQ ID NO: 35)

FIGURE 6A-3



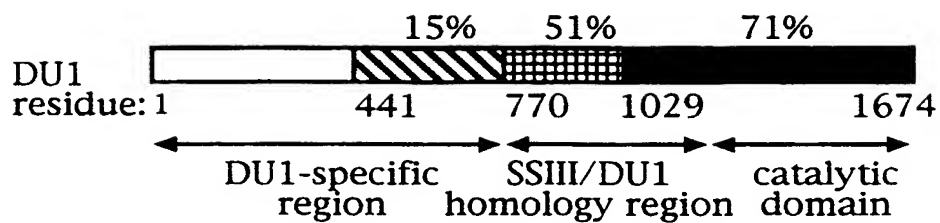


FIGURE 6B

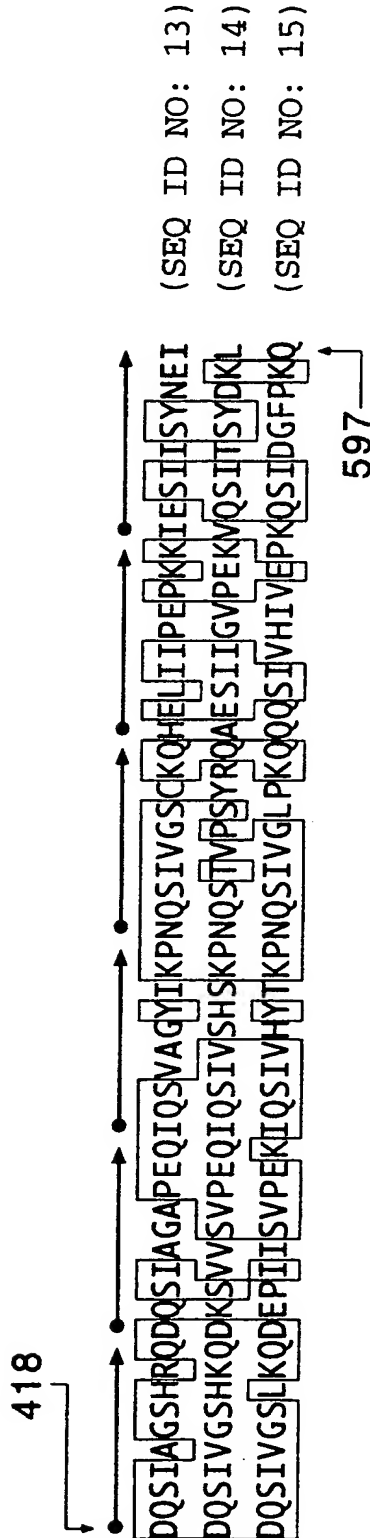
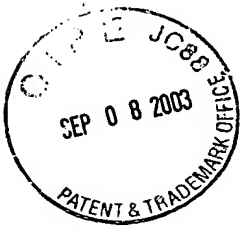
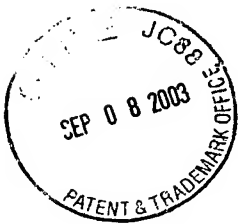


FIGURE 7A



SBE-repeats in DU1:

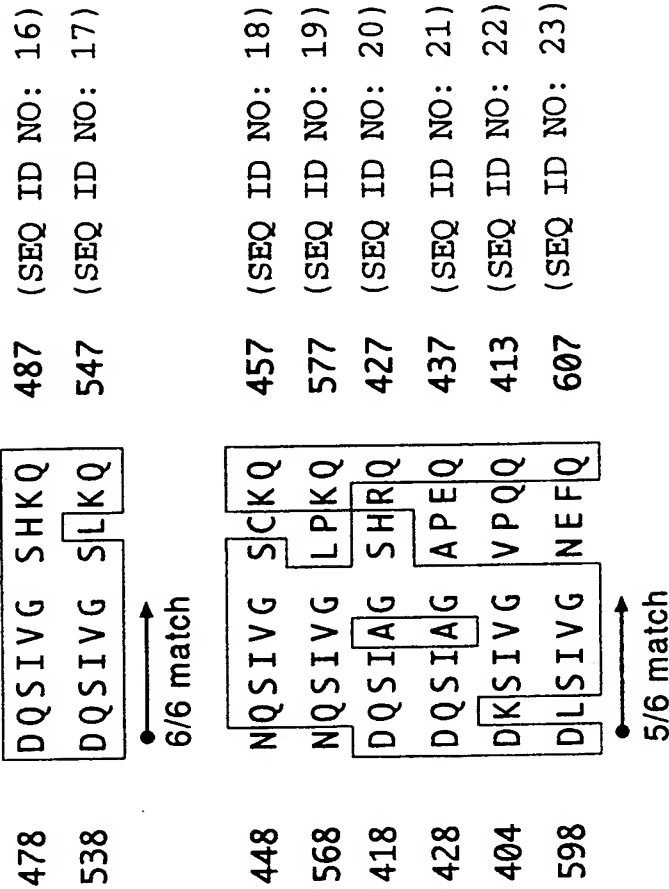


FIGURE 7B-1



SBEI family:

Maize SBEI	(SEQ ID NO: 24)
Pea SBEII	(SEQ ID NO: 25)
Wheat SBEI	(SEQ ID NO: 26)

529	*	*	553
KCIAYAESH	DQSIG	DKTIAFWLMD	
KCVSYAESH	DQSIG	DKTIAFWLMD	
KCIAYAESH	DQSIG	DKTMAFWLMD	

6/6 match

SBEII family:

Maize SBEIIa	(SEQ ID NO: 27)
Maize SBEIIb	(SEQ ID NO: 28)
Pea SBEI	(SEQ ID NO: 29)

572	*	*	596
KCVTYCESH	DQALVG	DKTIAFWLMD	
KCVTYAESH	DQALVG	DKTIAFWLMD	
KCVVYCESH	DQALVG	DKTLAFWLMD	

4/6 match

Glycogen branching enzymes:

Yeast GLC3	(SEQ ID NO: 30)
Human liver	(SEQ ID NO: 31)

477	*	*	501
KVVAICESH	DQALVG	DKSLAFWLMD	
KCIAYAESH	DQALVG	DKTLAFWLMD	

4/6 match

FIGURE 7B-2

150 → ETVDEAEVEEDK -- FEVDTSGLRNVAVR (SEQ ID NO: 32)  
 E - VDPKDEHNAKDV FVVDSSGTAPDNAAVE (SEQ ID NO: 33)  
 EVVDEAEVEEDM -- VDVDILGLDNLNATI ← 233 (SEQ ID NO: 34)

**FIGURE 7C**

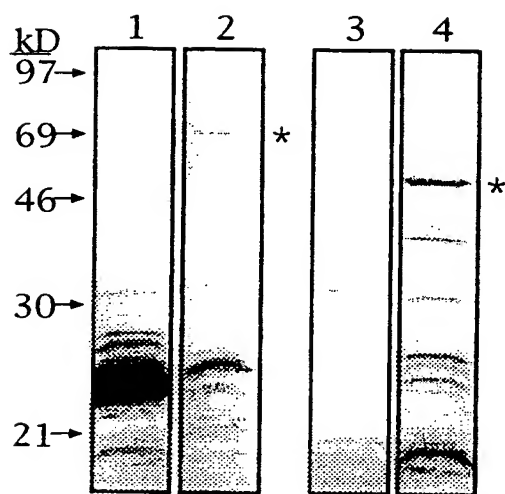


FIGURE 8

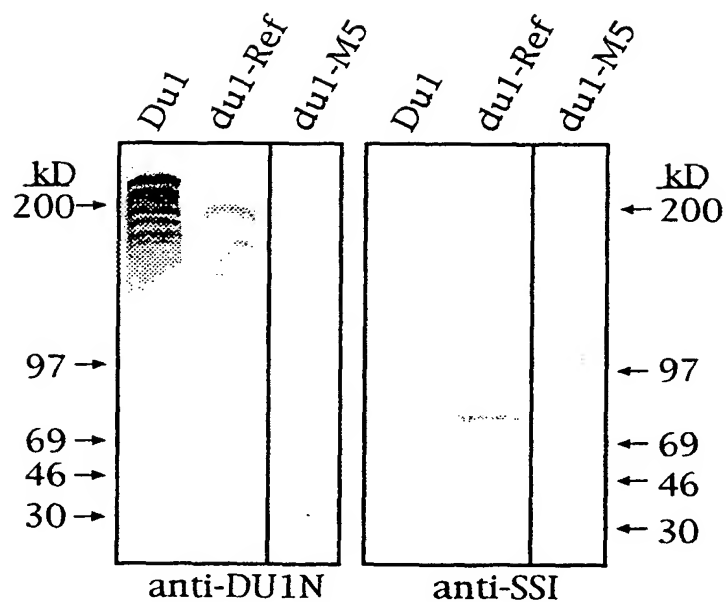


FIGURE 9A

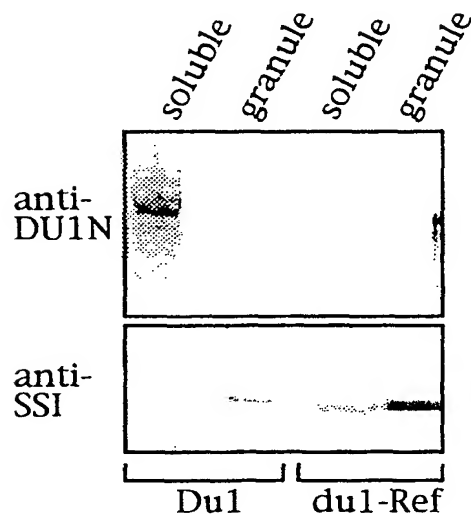


FIGURE 9B

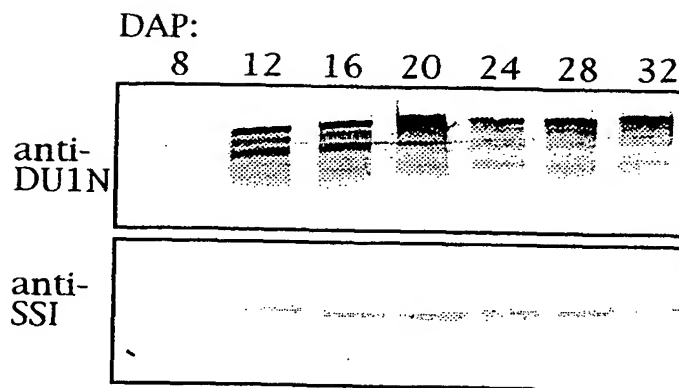


FIGURE 9C



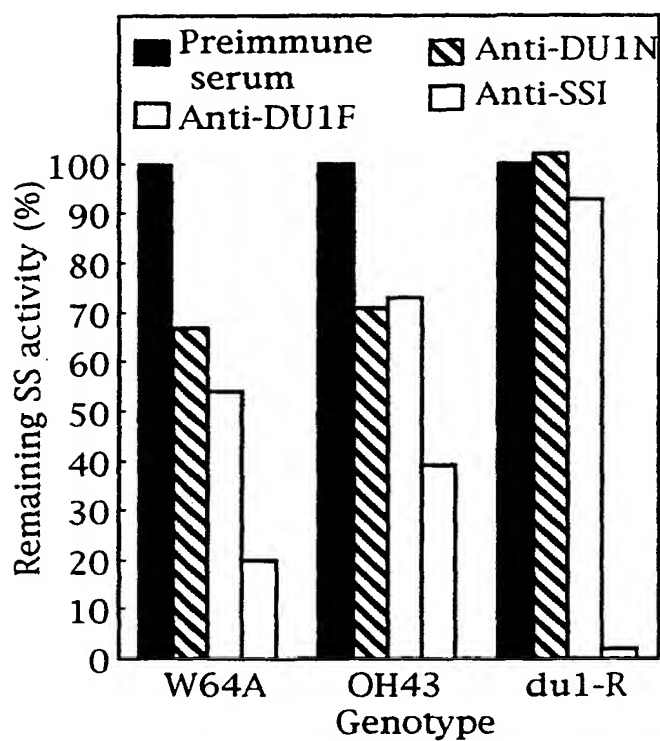


FIGURE 10

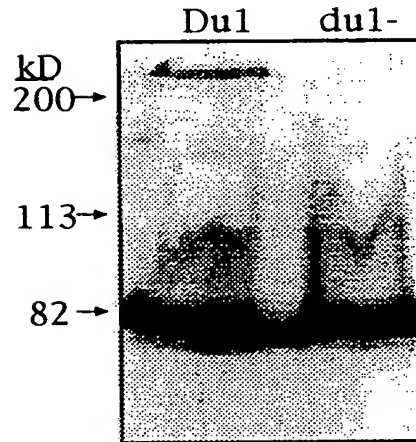


FIGURE 11A

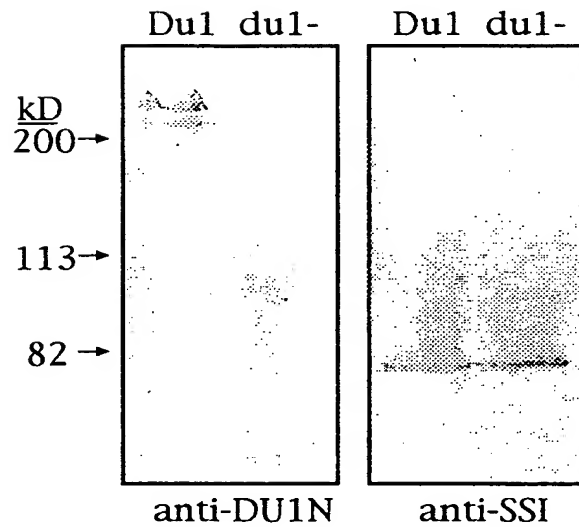


FIGURE 11B

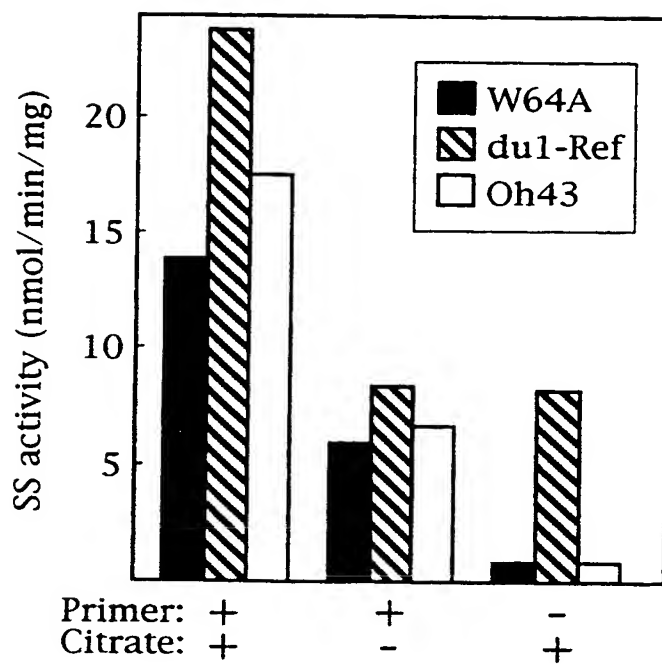


FIGURE 12